



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 144275

To: Nita M Minnifield
Location: REM 3C01/3C18
Art Unit: 1645
Friday, February 04, 2005

Case Serial Number: 09/837344

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

*Reviewed
2/7/05*

Shears, Beverly

144275

From: Minnifield, Nita 71976
Sent: Thursday, February 03, 2005 11:21 AM
To: Shears, Beverly
Subject: RE: sequence search request

09/837344

Beverly,
I checked the complete RSL and the previous search report, could you search SEQ ID NO: 31 and 20 (both aa) on commercial and interference databases.

Thanks,
Nita

-----Original Message-----

From: Shears, Beverly
Sent: Wednesday, February 02, 2005 10:33 AM
To: Minnifield, Nita
Subject: RE: sequence search request

Nita,

I apologize for the mix up. This query was searched against the AA dBS. Printing results now. Expect delivery by COB today.

Beverly

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, February 01, 2005 5:46 PM
To: Shears, Beverly
Subject: FW: sequence search request

Beverly,
Please run a commercial and interference search on the amino acid sequence of SEQ ID NO:41 against the aa databases. If I am not making the proper request please let me know how I should it for future reference.

Thanks,
Minnifield

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, January 11, 2005 9:51 AM
To: STIC-Biotech/ChemLib
Subject: sequence search request

STIC,

09/837344

Please do a commercial and interference
sequence search on SEQ ID NO: 41 of this
application.

1

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors--

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGN

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:13 ; Search time 37.9492 Seconds

(Without alignments)
801.190 Million cell updates/sec

Title: US-09-837-344-31

Sequence: 1 SDLEGRRAKXKLEQEQSDL.....GHLEKKQKSIKPEQKEDKS 316

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1494	95.6	1909	2	A45592
2	328	21.0	1407	1	S28589
3	318.5	20.4	737	2	T15597
4	318.5	20.4	1017	2	T15598
5	317.5	20.3	1898	1	A45973
6	310.5	19.9	1549	1	A40691
7	289	18.5	407	2	S23325
8	287.5	18.4	1432	2	B85431
9	283.5	18.1	451	2	G70241
10	272	17.4	699	2	E84565
11	271.5	17.4	887	2	G84884
12	269	17.2	402	2	S37046
13	269	17.2	1979	2	T50989
14	267.5	17.1	729	2	T50591
15	266	17.0	877	2	T27232
16	261.5	16.7	649	2	T150591
17	261	16.7	746	2	T47237
18	260.5	16.7	1166	2	H86341
19	260	16.6	771	1	A33430
20	259	16.6	1840	2	T29091
21	258.5	16.5	792	2	T42963
22	258	16.5	386	2	S05568
23	255.5	16.3	501	2	C71948
24	254.5	16.3	1961	1	MMK1231
25	254.5	16.3	1963	1	MMK1231
26	253.5	16.2	520	2	S35575
27	253.5	16.2	1039	2	S18199
28	253.5	16.2	1738	2	T14867
29	253	16.2	810	2	T44430

ALIGNMENTS

RESULT 1

A45592

liver stage antigen LSA-1 - malaria parasite (Plasmodium falciparum)

C/Date: 22-Nov-1993 #sequence revision 02-Dec-1994 #text change 09-Jul-2004

C/Accession: S24597; A45592; S29393; S34842; B45592; C45592; D45592

R/Zhu, J.; Hollingdale, M. submitted to the EMBL Data Library, November 1990

A/Reference number: S24597

A/Accession: S24597

A/Molecule type: DNA

A/Residues: 1-1909 <ZHU>

A/Cross-references: UNIPROT:Q25893; EMBL:X56203; NID:G9915; PID:G9916

R/Zhu, J.; Hollingdale, M. R. Mol. Biochem. Parasitol. 48: 223-226, 1991

A/Title: Structure of Plasmodium falciparum liver stage antigen-1.

A/Reference number: A45592; MUID:92107224; PMID:1840628

A/Accession: A45592

A/Molecule type: DNA

A/Residues: 1-195;638-688;1165-1215;1590-1909 <ZH>

A/Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, N

R/Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Pataraotikul, J.; Beaudouin

Nature 329, 164-167, 1987

A/Title: A liver-stage-specific antigen of Plasmodium falciparum characterized by gene

A/Reference number: S29393; MUID:87315391; PMID:3306406

A/Accession: S29393

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 323-387 <GUE1>

A/Cross-references: EMBL:M28266

R/Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Pataraotikul, J.; Beaudouin

submitted to the EMBL Data Library, April 1992

myosin heavy chain
nuclear mitotic ap
hypothetical prote
myosin heavy chain
nonmuscle myosin I
probable erythrocy
emm L 15 protein -
M-1like protein emm
NF-180 - sea lamp
class I INCENP pro
myosin heavy chain
myosin heavy chain
involucrin - pig
myosin alpha heavy
myosin heavy chain
hypothetical colle

Query Match 95.6%; Score 1494; DB 2; Length 1909;
Beet Local Similarity 95.9%; Pred. No. 2.9e-60;
Matches 303; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
1 SDLEGRRAKXKLEQEQSDLEQDRLAKKLEQEQSDLEQRRRAKXKLEQEQSDLEQRRRA 60
DB 1421 SDLEGRRAKXKLEQEQSDLEQRRRAKXKLEQEQSDLEQRRRAKXKLEQEQSDLEQRRRA 1480

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 4, 2005, 10:45:37 ; Search time 490.42 Seconds
(without alignments)
209,865 Million cell updates/sec

Title: US-09-837-344-31

Sequence: 1 SDLEGERRAKELQEQSDL.....GHLEKXGSIKPEQEDKS 316

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.dep.*

2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.dep.*

3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.dep.*

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6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.dep.*

7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.dep.*

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9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.dep.*

10: /cgn2_6/ptodata/2/pubppa/US09B_PUBCOMB.dep.*

11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.dep.*

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13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.dep.*

14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.dep.*

15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.dep.*

16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.dep.*

17: /cgn2_6/ptodata/2/pubppa/US10D_NEW_PUB.dep.*

18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.dep.*

19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.dep.*

20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1563	100.0	316 9 US-09-837-344-31	Sequence 31, Appl
2	1563	100.0	316 10 US-09-900-963-31	Sequence 31, Appl
3	603	38.6	117 9 US-09-837-344-20	Sequence 20, Appl
4	603	38.6	117 10 US-09-900-963-20	Sequence 20, Appl
5	554	35.4	107 9 US-09-837-344-19	Sequence 19, Appl
6	554	35.4	107 10 US-09-900-963-19	Sequence 19, Appl
7	329.5	21.1	1439 17 US-10-754-079-157	Sequence 157, Appl
8	327.5	21.0	1162 11 US-09-884-273-2	Sequence 2, Appl
9	327.5	21.0	1162 14 US-10-284-804-2	Sequence 2, Appl
10	326	20.9	611 9 US-09-216-393-81	Sequence 81, Appl
11	326	20.9	611 14 US-10-321-856-81	Sequence 81, Appl
12	320	20.5	350 13 US-10-101-487-58	Sequence 58, Appl
13	311	19.9	621 15 US-10-108-260A-4409	Sequence 4409, Ap

14	307	19.6	240 13 US-10-101-487-75	Sequence 75, Appl
15	288	18.4	650 15 US-10-104-047-3636	Sequence 3636, Ap
16	282	18.0	466 15 US-10-108-260A-4344	Sequence 4344, Ap
17	280.5	17.9	345 14 US-10-029-386-34255	Sequence 34255, A
18	278	17.8	280 15 US-10-104-047-3063	Sequence 3063, Ap
19	277	17.7	735 15 US-10-144-194A-109	Sequence 109, App
20	277	17.7	784 15 US-10-144-194A-108	Sequence 108, App
21	277	17.7	843 15 US-10-144-194A-84	Sequence 84, Appl
22	275	17.6	779 15 US-10-144-194A-86	Sequence 86, Appl
23	273	17.5	507 15 US-10-425-114-47285	Sequence 47285, A
24	273	17.5	696 15 US-10-424-599-196058	Sequence 196058,
25	272	17.4	1170 15 US-10-341-434-95	Sequence 95, Appl
26	272	17.4	1564 15 US-10-144-198-2	Sequence 2, Appl
27	272	17.4	1564 15 US-10-144-198-50	Sequence 4, Appl
28	268	17.1	187 13 US-10-101-487-50	Sequence 50, Appl
29	268	17.1	798 15 US-10-104-047-3335	Sequence 335, Ap
30	264	16.9	336 17 US-10-754-079-158	Sequence 158, App
31	261.5	16.7	1709 13 US-10-101-487-53	Sequence 53, Appl
32	261	16.7	179 13 US-10-101-487-46	Sequence 46, Appl
33	261	16.7	186 13 US-10-101-487-44	Sequence 44, Appl
34	261	16.7	191 13 US-10-101-487-81	Sequence 81, Appl
35	260.5	16.7	198 13 US-10-101-487-42	Sequence 42, Appl
36	260.5	16.7	287 14 US-10-029-386-33041	Sequence 33041, A
37	259.5	16.6	267 15 US-10-424-599-196057	Sequence 196057,
38	259	16.6	181 13 US-10-101-487-45	Sequence 45, Appl
39	258	16.5	197 13 US-10-101-487-114	Sequence 114, App
40	257	16.4	176 13 US-10-101-487-70	Sequence 70, Appl
41	256	16.4	177 13 US-10-101-487-48	Sequence 48, Appl
42	256	16.4	177 13 US-10-101-487-115	Sequence 115, Appl
43	255.5	16.3	501 15 US-10-335-977-8259	Sequence 8259, Ap
44	255.5	16.3	505 15 US-10-335-977-8260	Sequence 8260, Ap
45	255.5	16.3	1960 15 US-10-236-031B-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-09-837-344-31

Sequence 31, Application US/09837344

Patent No. US20020041882A1

GENERAL INFORMATION:

APPLICANT: GUERIN-MARCHAND, Claudine

DRUIHE, Pierre

TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE

HEPATITC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE

OF STIMULATING THE T LYMPHOCYTES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/837,344

FILING DATE: 19-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/462,625

FILING DATE: <Unknown>

APPLICATION NUMBER: FR 91 01286

FILING DATE: 05-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: McDowman, Malcolm K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 010830-078

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 ; Search time 42.3279 Seconds
(without alignments)
495.098 Million cell updates/sec

Title: US-09-837-344-31

Perfect score: 1563
Sequence: 1 SLDGERAKRKLQGGQSDL.....GHLEKKGSGIKPEQKDKS 316

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1563	100.0	316	3 US-08-098-327E-31	Sequence 31, Appl
2	1563	100.0	316	3 US-08-462-625-31	Sequence 31, Appl
3	603	38.6	117	3 US-08-098-327E-20	Sequence 20, Appl
4	603	38.6	117	3 US-08-462-625-20	Sequence 20, Appl
5	554	35.4	107	3 US-08-098-327E-19	Sequence 19, Appl
6	344	22.0	608	4 US-08-462-625-19	Sequence 19, Appl
7	344	22.0	608	4 US-09-270-767-32937	Sequence 32937, A
8	327.5	21.0	1162	2 US-08-728-323A-2	Sequence 48154, A
9	327.5	21.0	1162	2 US-09-298-568-2	Sequence 2, Appl
10	327.5	21.0	1162	4 US-09-410-399-2	Sequence 2, Appl
11	327.5	21.0	1162	4 US-09-894-273-2	Sequence 2, Appl
12	327.5	21.0	1162	4 US-09-216-393B-81	Sequence 81, Appl
13	326	20.9	611	4 US-08-056-200-94	Sequence 94, Appl
14	317.5	20.3	1898	2 US-08-800-644-94	Sequence 94, Appl
15	317.5	20.3	1898	2 US-09-538-092-1280	Sequence 1280, Ap
16	317.5	20.3	1898	2 US-09-543-681A-6436	Sequence 6436, Ap
17	301	19.3	1180	4 US-10-164-595-80	Sequence 80, Appl
18	277	17.7	784	4 US-10-164-595-79	Sequence 79, Appl
19	277	17.7	784	4 US-10-164-595-54	Sequence 54, Appl
20	275	17.6	779	4 US-09-270-767-44900	Sequence 56, Appl
21	265	17.0	676	4 US-09-248-796A-14503	Sequence 14503, A
22	260	16.6	1402	4 US-09-543-681A-6012	Sequence 6012, Ap
23	259	16.6	613	4 US-09-538-092-1077	Sequence 1077, Ap
24	255	16.3	1960	4 US-08-466-390-4	Sequence 4, Appl
25	255	16.3	683	6 US-08-466-390-4	Sequence 4, Appl
26	253	16.2	2101	1 US-08-470-950-4	Sequence 4, Appl
27	253	16.2	2101	1 US-08-467-781-4	Sequence 4, Appl

28	253	16.2	2101	1 US-08-470-950-4	Sequence 4, Appl
29	253	16.2	2101	1 US-08-467-781-4	Sequence 4, Appl
30	253	16.2	2101	1 US-08-195-487-4	Sequence 4, Appl
31	253	16.2	2101	2 US-08-483-924-4	Sequence 1, Appl
32	253	16.2	2101	3 US-09-452-294-1	Sequence 4, Appl
33	253	16.2	2101	5 PCT-US93-06160-4	Sequence 4, Appl
34	250.5	16.0	1976	4 US-09-538-092-1078	Sequence 1078, Ap
35	247.5	15.8	1937	4 US-09-538-092-918	Sequence 918, Ap
36	247.5	15.8	1939	3 US-09-310-187A-1	Sequence 1, Appl
37	247.5	15.8	1939	4 US-09-538-092-917	Sequence 917, Ap
38	246	15.7	1972	4 US-08-875-435B-4	Sequence 4, Appl
39	245.5	15.7	1239	4 US-09-688-188B-13	Sequence 13, Appl
40	245.5	15.7	1239	4 US-09-291-417D-13	Sequence 13, Appl
41	245.5	15.7	1972	4 US-08-875-435B-3	Sequence 3, Appl
42	244.5	15.6	1866	3 US-08-938-105-3	Sequence 3, Appl
43	244	15.6	235	4 US-09-270-767-36681	Sequence 36681, A
44	244	15.6	235	4 US-09-270-767-51898	Sequence 51898, A
45	244	15.6	793	4 US-09-538-092-1271	Sequence 1271, Ap

ALIGNMENTS

RESULT 1
US-08-098-327E-31
Sequence 31, Application US/08098327E

Patent No. 6270771

GENERAL INFORMATION:

APPLICANT: GUERIN-MARCHAND, Claudine

APPLICANT: DRULHE, Pierre

TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE

TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPIOTOPS CAPABLE

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/098,327E

FILING DATE: 24-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 01286

FILING DATE: 05-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: McGowan, Malcolm K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 010830-045

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 316 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PUBLICATION INFORMATION:

DOCUMENT NUMBER: WO 92/13884

PUBLICATION DATE: 20-AUG-1992

US-08-098-327E-31

Query Match 100.0%, Score 1563, DB 3, Length 316;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 ; Search time 91.9518 seconds
(without alignments)
1232.776 Million cell updates/sec

Title: US-09-837-344-31

Perfect score: 1563
Sequence: 1 SLEGEERRAKETLQEQQSDL.....GHLEKXKDGSIKPEKEDKS 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: geneeqp19908:*
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4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038:*
7: geneeqp20038:*
8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1549	99.1	493	AA26944	Aar26944 P.falcipa
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4	771.5	49.4	318	AA26943	Aar26943 P.falcipa
5	739	47.3	456	AD021942	Ado21942 LSA-NRC(H
6	739	47.3	457	AD021920	Ado21920 LSA-NRC(H
7	603	38.6	117	AA26937	Aar26937 P.falcipa
8	331	21.2	207	AA844672	Aar44672 Gene 33 h
9	327.5	21.0	1162	AA596255	Aay96255 Kaposi's
10	327.5	21.0	1162	AA596255	Aay96255 Kaposi's
11	327.5	21.0	1162	AA596255	Aay96255 Kaposi's
12	327.5	21.0	1162	AA596255	Aay96255 Kaposi's
13	327.5	21.0	1162	AA596255	Aay96255 Kaposi's
14	326	20.9	611	AA26939	Aar26939 P.falcipa
15	326	20.9	611	AA26939	Aar26939 P.falcipa
16	326	20.9	611	AA26939	Aar26939 P.falcipa
17	321	20.5	360	AA03627	Aa03627 Human fol
18	321	20.5	412	AA03626	Aa03626 Human fol
19	321	20.5	554	AB859454	Ab859454 Drosophi
20	317.5	20.3	1898	AA30795	Aay30795 A human c
21	317.5	20.3	1898	AA30795	Aay30795 A human c
22	312	20.0	345	AB053267	Ab053267 Human tes
23	311	19.9	621	AD005724	Ad005724 Human tes
24	306	19.6	2274	AB85657	Ab85657 Drosophi
25	302.5	19.4	562	AA70491	Aar70491 Leucocyto

26	301	19.3	1180	7	ADP06151	Adp06151 Bacterial
27	296.5	19.0	2990	8	ADP29884	Adp29884 Human sec
28	289	18.5	407	8	ADP49328	Adp49328 S pyrogen
29	289	18.5	923	4	ABG08600	Abg08600 Novel hum
30	288	18.4	650	7	ADB65482	Adb65482 Human pro
31	288	18.4	949	4	ABG15508	Abg15508 Novel hum
32	285	18.2	1940	8	ADP29883	Adp29883 Human sec
33	284	18.2	67	1	AA81355	Aa81355 Sequence
34	284	18.2	1715	4	AB858089	Ab858089 Drosophi
35	282	18.0	466	7	AD005659	Ad005659 Human pro
36	281	18.0	658	4	AB856532	Ab856532 Drosophi
37	281	18.0	800	4	AB871459	Ab871459 Drosophi
38	280.5	17.9	345	8	AB060621	Ab060621 Human gen
39	278	17.8	280	7	ADB64809	Adb64809 Human pro
40	277	17.7	695	4	AAW79466	Aaw79466 Human pro
41	277	17.7	735	6	AB858340	Ab858340 AAC97961
42	277	17.7	735	6	ADK65841	Adk65841 Angiogene
43	277	17.7	784	6	AB858339	Ab858339 AAF19255
44	277	17.7	784	6	AB052982	Ab052982 Human put
45	277	17.7	784	7	ADK65840	Adk65840 Angiogene

ALIGNMENTS

RESULT 1

AA26941
ID AAR26941 standard; protein; 316 AA.

AA26941;

25-MAR-2003 (revised)
08-FEB-1993 (first entry)

P.falciparum LSA-R-NR protein.

Malaria; hepatocyte; sporozoite; plasmid DG 536; T-cell epitope;
palladium; liver stage-specific antigen.

Plasmodium falciparum.

Key Location/Qualifiers

Region 1..209
/label= repeat_region
/note= "contains 12 x 17mer repeats"
210..316
/label= non-repeat_region

MO9213884-A1.

20-AUG-1992.

05-FEB-1992; 92MO-FR000104.

05-FEB-1991; 91FR-00001286.

(INSP) INST PASTEUR.

Guerinmarchand C, Drulhe P;

WPI, 1992-299985/36.

N-PSDB; AAQ28115.

Polypeptide(s) derived from liver stage of PLASMODIUM FALCIPARUM - for
vaccination against, treatment of and diagnosis of malaria.

Disclosure; Fig 1; 81pp; French.

A genomic DNA bank of P.falciparum EcoRI fragments prepared in lambda
gt10 was used to transform E.coli. The expression library was screened
with human antisera against antigens of all stages of P. falciparum. The
library was rescreened with antibodies affinity-purified on a clone
which was able to recognise antibodies specific to the hepatic phase.

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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 ; Search time 33.5058 Seconds

(without alignments)
2009.171 Million cell updates/sec

Title: US-09-837-344-20

Sequence: 1 LQEQRDLEQRKADTKKLE.....GHLEKKDGSIKPEQKEDKS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	100.0	493	2	Q25886
2	602	99.8	1909	2	Q25893
3	597	99.0	1596	2	Q25893
4	554	91.9	280	2	Q25844
5	554	91.9	280	2	Q25849
6	554	91.9	280	2	Q25850
7	553	91.7	280	2	Q25843
8	553	91.7	280	2	Q25846
9	553	91.7	280	2	Q25847
10	553	91.7	280	2	Q25851
11	550	91.2	280	2	Q25848
12	550	91.2	280	2	Q25852
13	549	91.0	280	2	Q25845
14	549	91.0	280	2	Q25853
15	549	91.0	280	2	Q25854
16	549	91.0	280	2	Q25855
17	549	91.0	280	2	Q25856
18	549	91.0	280	2	Q25857
19	549	91.0	280	2	Q25858
20	549	91.0	280	2	Q25859
21	469	91.0	280	2	Q25900
22	469	91.0	280	2	Q25900
23	469	91.0	280	2	Q25900
24	469	91.0	280	2	Q25900
25	469	91.0	280	2	Q25900
26	469	91.0	280	2	Q25900
27	469	91.0	280	2	Q25900
28	469	91.0	280	2	Q25900
29	469	91.0	280	2	Q25900
30	469	91.0	280	2	Q25900
31	469	91.0	280	2	Q25900

32	89.5	14.8	295	2	Q6BXX9	06bxx9 debaryomyce
33	89.5	14.8	485	2	Q7SEU2	07seu2 ashyia gose
34	89.5	14.8	485	2	AA550359	AA550359 ashyia go
35	89.5	14.8	6328	2	Q8MNS0	Q8mns0 caenorhabdi
36	89.5	14.8	18519	2	Q8ISF6	Q8isf6 caenorhabdi
37	89.5	14.8	18534	2	Q8ISF7	Q8isf7 caenorhabdi
38	88	14.6	217	2	Q6QTF7	Q6qtf7 solanum tub
39	88	14.6	217	2	AA517876	AA517876 solanum t
40	88	14.6	710	2	Q7RJN5	Q7rjn5 plasmodium
41	88	14.6	791	2	Q22142	Q22142 caenorhabdi
42	87.5	14.5	282	1	NSB1_HUMAN	NSB1_HUMAN
43	87.5	14.5	1418	2	Q86HT4	Q86ht4 dictyostel
44	87	14.4	535	2	Q44192	Q44192 caenorhabdi
45	87	14.4	650	2	Q7RCN9	Q7rcn9 plasmodium

ALIGNMENTS

RESULT 1

Q25886

ID Q25886 PRELIMINARY; PRT; 493 AA.

AC Q25886; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

OS Name=LSA-1; Plasmodium falciparum liver stage antigen-1 (Fragment).

GN Name=LSA-1; Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5833;

RN (1) MEDLINE=94267224; PubMed=7515922;

RA Fidoek D.A., Gras-Masse H., Lepers J., Brahimi K., Benmohamed L.,

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RA Fidoek D.A., Gras-Masse H., Lepers J., Brahimi K., Benmohamed L.,

RA Fidoek D.A., Gras-Masse H., Lepers J., Brahimi K., Benmohamed L.,

QY	1	LOEQRDLEQRKADTKKLEKKHGDILAEYGRLEPALEPSSENGGYVPHOSL 60
DB	204	LQEQRDLEQRKADTKKLEKKHGDILAEYGRLEPALEPSSENGGYVPHOSL 263
QY	61	PODRKNSRDSKSEISIEKTNRRESITTVNVEGRDINHGHLEKKDGSIKPEQKEDKS 117
DB	264	PODRKNSRDSKSEISIEKTNRRESITTVNVEGRDINHGHLEKKDGSIKPEQKEDKS 320

Query Match: 100.0%; Score 603; DB 2; Length 493;

Best Local Similarity: 100.0%; Pred. No. 2, 8e-42;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Q25893

ID Q25893 PRELIMINARY; PRT; 1909 AA.

AC Q25893; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

OS Liver stage antigen.

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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:13 ; Search time 14.0508 Seconds
(without alignments)
801.190 Million cell updates/sec

Title: US-09-837-344-20

Perfect score: 603
Sequence: 1 LQEQQRDLQRKADTKNLE.....GLHEKKQGSIKPEQKEDKS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	99.8	1909	2 A45592	liver stage antigen
2	102	16.9	210	2 C70309	transcription regu
3	94.5	15.7	772	2 I50463	protein kinase - c
4	91.5	15.2	635	1 S5352	involucrin L - gor
5	90.5	15.0	1085	2 S5352	IFM1 protein - yea
6	90	14.9	756	2 T00367	hypothetical prote
7	89.5	14.8	3488	2 T34418	hypothetical prote
8	88	14.6	762	2 G88436	protein T04A.13 l
9	87	14.6	791	2 T24335	hypothetical prote
10	87	14.4	779	2 T23560	hypothetical prote
11	87	14.4	779	2 E34024	hypothetical prote
12	84.5	14.0	585	1 A24168	protein kinase (EC
13	84.5	14.0	605	1 A24168	involucrin - human
14	84.5	14.0	765	1 ISHUT1	involucrin M - gor
15	84	13.9	913	2 T52485	DNA topoisomerase
16	83.5	13.8	615	2 T66108	neurofilament prot
17	83.5	13.8	789	2 T51310	hypothetical prote
18	83.5	13.8	821	2 S67087	RNA helicase RH28
19	83.5	13.8	1025	2 A47453	hypothetical prote
20	83.5	13.8	1706	2 T29305	transcription fact
21	83	13.8	483	2 S41853	protein kinase - f
22	83	13.8	684	2 S52835	centromere/microtu
23	82.5	13.7	495	1 I37062	hypothetical prote
24	82.5	13.7	1027	1 I37062	involucrin S - gor
25	81.5	13.5	442	2 D70315	kinesin heavy chai
26	81.5	13.5	980	2 E71606	transcription regu
27	81.5	13.5	1829	2 T26135	hypothetical prote
28	81	13.4	543	2 T32973	hypothetical prote
29	81	13.4	1390	2 T14004	citr protein - sll

30	80.5	13.3	678	2 A54514	glutamic acid-rich
31	80.5	13.3	768	2 H54024	protein kinase (EC
32	80.5	13.3	777	2 B54024	protein kinase (EC
33	80.5	13.3	1032	2 T34510	neutonal kinesin h
34	80.5	13.3	1804	2 T34518	neutrin - golden ha
35	80	13.3	452	2 D64583	hypothetical prote
36	80	13.3	729	2 T50989	hypothetical prote
37	79.5	13.2	501	2 C71948	hypothetical prote
38	79.5	13.2	816	2 S64439	hypothetical prote
39	79.5	13.2	1132	2 T43483	translacton initia
40	79.5	13.2	1203	2 S26650	DNA-binding protei
41	79.5	13.2	1840	2 T29091	transititin - chic
42	79	13.1	511	2 H83339	probable transcrip
43	79	13.1	630	2 S29796	hypothetical prote
44	79	13.1	721	2 S29795	hypothetical prote
45	79	13.1	783	2 A55817	cyclin-dependent k

ALIGNMENTS

RESULT 1
A45592
liver stage antigen LGA-1 - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 22-Nov-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: S24597; A45592; S29393; S34842; B45592; C45592; D45592
R:Zhu, J.; Hollingdale, M.
Submitted to the EMBL Data Library, November 1990
A:Reference number: S24597
A:Accession: S24597
A:Molecule type: DNA
A:Residues: 1-1909 <ZHU>
A:Cross-references: UNIPROT:Q25893; EMBL:X56203; NID:93915; PID:93916
R:Zhu, J.; Hollingdale, M.R.
Mol. Biochem. Parasitol. 48, 223-226, 1991
A:Title: Structure of Plasmodium falciparum liver stage antigen-1.
A:Reference number: A45592; MUID:92107224; PMID:1840628
A:Accession: A45592
A:Molecule type: DNA
A:Residues: 1-195;638-688;1165-1215;1590-1909 <ZH2>
A:Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, X
R:Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Pataportikul, J.; Beaudot
Nature 329, 164-167, 1987
A:Title: A liver-stage-specific antigen of Plasmodium falciparum characterized by gene
A:Reference number: S29393; MUID:87315391; PMID:3306406
A:Accession: S29393
A:Molecule type: DNA
A:Status: Preliminary
A:Residues: 323-387 <GUE1>
A:Cross-references: EMBL:M28266
R:Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Pataportikul, J.; Beaudot
submitted to the EMBL Data Library, April 1992
A:Description: a liver-stage-specific antigen of plasmodium falciparum characterized by
A:Reference number: S34842
A:Accession: S34842
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 323-381, 'HKA1' <GUE2>
A:Cross-references: EMBL:M28266
A:Note: difference at carboxyl end due to frameshift error
C:Comment: This protein is found as flocculent material in the parasitophorous vacuole.
C:Superfamily: trichonyalin calmodulin repeat homology
C:Keywords: EF hand
F:154-1629/Region: 17-residue repeats (A-K-E-K-L-Q-E-O-Q-S-D-L-E-Q-E-R-R)
Query Match 99.8%; Score 602; DB 2; Length 1909;
Best Local Similarity 99.1%; Pred. No. 2.2e-43;
Matches 116; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQEQQRDLQRKADTKNLEKKHGDI LAEDLYGRLEIPALISPSENERGYIIPHOSSL 60
Db 1620 LQEQQRDLQRKADTKNLEKKHGDI LAEDLYGRLEIPALISPSENERGYIIPHOSSL 1679

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OM protein - protein search, using sw model

Run on: February 4, 2005, 10:45:37 ; Search time 181.58 Seconds
(without alignments)
209.865 Million cell updates/sec

Title: US-09-837-344-20
Perfect score: 603
Sequence: 1 LQEQGRDLQKADTKKMLE.....GHLEKKGSIRPEQKEDKS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Publications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	100.0	117	9	US-09-837-344-20
2	603	100.0	117	9	US-09-900-963-20
3	603	100.0	316	9	US-09-837-344-31
4	603	100.0	316	10	US-09-900-963-31
5	554	91.9	107	9	US-09-837-344-19
6	554	91.9	107	10	US-09-900-963-19
7	154	25.5	31	9	US-09-837-344-23
8	154	25.5	31	10	US-09-900-963-23
9	141	23.4	27	9	US-09-837-344-21
10	141	23.4	27	10	US-09-900-963-21
11	94	13.6	456	9	US-09-894-018-121
12	89.5	14.8	231	9	US-09-922-261-194
13	89.5	14.8	232	9	US-09-922-261-192

14	89.5	14.8	238	9	US-09-922-261-190	Sequence 190, App
15	89.5	14.8	257	9	US-09-922-261-188	Sequence 188, App
16	89.5	14.8	272	9	US-09-922-261-186	Sequence 186, App
17	87	14.4	550	15	US-10-369-493-5995	Sequence 5995, Ap
18	85.5	14.2	765	10	US-09-882-274-2	Sequence 2, Appl
19	85.5	14.2	765	16	US-10-408-765A-1149	Sequence 1149, Ap
20	85	14.1	15	13	US-10-103-395-74	Sequence 74, Appl
21	84	13.9	24	9	US-09-837-344-22	Sequence 22, Appl
22	84	13.9	24	10	US-09-900-963-22	Sequence 22, Appl
23	83.5	13.8	257	15	US-10-425-114-58860	Sequence 58860, A
24	83.5	13.8	395	15	US-10-425-114-59744	Sequence 59744, A
25	83.5	13.8	903	15	US-10-282-122A-52328	Sequence 52328, A
26	83	13.8	2683	16	US-10-437-663-185370	Sequence 185370, A
27	82.5	13.7	1027	14	US-10-080-608A-27	Sequence 27, Appl
28	82.5	13.7	1027	15	US-10-370-685-116	Sequence 116, App
29	82.5	13.7	1264	15	US-10-369-493-3742	Sequence 3742, Ap
30	82	13.6	472	10	US-09-953-407-2	Sequence 2, Appl
31	82	13.6	1429	10	US-09-953-407-1	Sequence 1, Appl
32	81.5	13.5	485	10	US-09-769-736-72	Sequence 72, Appl
33	81	13.4	294	15	US-10-425-114-59118	Sequence 49118, A
34	81	13.4	396	15	US-10-424-599-168151	Sequence 168151, A
35	81	13.4	542	15	US-10-424-599-234091	Sequence 234091, A
36	80.5	13.3	1032	14	US-10-080-608A-26	Sequence 26, Appl
37	80.5	13.3	1032	15	US-10-370-685-115	Sequence 115, App
38	80	13.3	452	9	US-09-881-752A-268	Sequence 268, App
39	80	13.3	452	15	US-10-282-122A-58723	Sequence 58723, A
40	79.5	13.2	321	9	US-09-864-761-33718	Sequence 33718, A
41	79.5	13.2	361	9	US-09-864-761-33614	Sequence 33614, A
42	79.5	13.2	361	9	US-09-864-761-34141	Sequence 34141, A
43	79.5	13.2	501	15	US-10-335-977-8259	Sequence 8259, Ap
44	79.5	13.2	505	15	US-10-335-977-8260	Sequence 8260, Ap
45	79.5	13.2	886	15	US-10-260-708-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-837-344-20
Sequence 20, Application US/09837344
Patent No. US20020041882A1
GENERAL INFORMATION:
APPLICANT: GUERIN-MARCHAND, Claudine
DRUILHE, Pierre
TITLE OF INVENTION: HEPATIC SEQUENCES SPECIFIC FOR THE
HEPATITIS STAGES OF P. FALCIPARUM BEARING EPIITOPS CAPABLE
OF STIMULATING THE T LYMPHOCYTES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/837,344
FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,625
FILING DATE: <Unknown>
APPLICATION NUMBER: FR 91 01286
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-078

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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 (Search time 15.6721 Seconds
(without alignments)
495.098 Million cell updates/sec

Title: US-09-837-344-20

Perfect score: 603
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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3: /cgn2_6/prodata/1/1aa/5R COMB pep.*
4: /cgn2_6/prodata/1/1aa/6B COMB pep.*
5: /cgn2_6/prodata/1/1aa/6R COMB pep.*
6: /cgn2_6/prodata/1/1aa/6CTUS COMB pep.*
7: /cgn2_6/prodata/1/1aa/6CTUS COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	100.0	117	3	US-08-098-327E-20
2	603	100.0	117	3	US-08-462-625-20
3	603	100.0	117	3	US-08-462-625-20
4	603	100.0	117	3	US-08-098-327E-31
5	603	100.0	117	3	US-08-462-625-31
6	554	91.9	107	3	US-08-098-327E-19
7	554	91.9	107	3	US-08-462-625-19
8	154	25.5	31	3	US-08-098-327E-23
9	154	25.5	31	3	US-08-462-625-23
10	141	23.4	27	3	US-08-098-327E-21
11	141	23.4	27	3	US-08-462-625-21
12	111	16.1	709	4	US-09-248-796A-19045
13	90.5	15.0	1085	1	US-08-431-080-28
14	90.5	15.0	1085	2	US-08-338-534-28
15	89.5	14.8	1085	3	US-09-345-294-28
16	89.5	14.8	231	3	US-09-461-697-194
17	89.5	14.8	232	3	US-09-461-697-192
18	89.5	14.8	237	3	US-09-461-697-190
19	89.5	14.8	258	3	US-09-461-697-188
20	86	14.3	272	3	US-09-461-697-186
21	86	14.3	457	4	US-09-710-279-2900
22	85.5	14.2	765	4	US-09-538-092-906
23	85	14.1	15	4	US-09-009-953-74
24	84.5	14.0	150	3	US-09-395-689-2
25	84.5	14.0	300	3	US-09-395-689-1
26	84.5	14.0	765	2	US-08-663-112-2
27	84	13.9	24	3	US-08-098-327E-22

28	84	13.9	24	3	US-08-462-625-22	Sequence 22, Appl
29	84	13.9	1761	4	US-09-561-709B-1	Sequence 1, Appl
30	83.5	13.8	1025	4	US-09-538-092-334	Sequence 334, App
31	82.5	13.7	1027	4	US-09-914-259-27	Sequence 27, Appl
32	80.5	13.3	129	4	US-09-513-999C-5707	Sequence 5707, Appl
33	80.5	13.3	1032	4	US-09-914-259-26	Sequence 26, Appl
34	80.5	13.3	1032	4	US-09-538-092-1293	Sequence 1293, App
35	79	13.1	140	4	US-09-710-279-2288	Sequence 2288, App
36	79	13.1	140	4	US-09-710-279-2288	Sequence 2438, App
37	79	13.1	147	3	US-09-134-001C-5518	Sequence 5518, App
38	79	13.1	538	4	US-09-252-991A-23551	Sequence 23551, A
39	79	13.1	708	3	US-08-235-836C-76	Sequence 76, Appl
40	78	12.9	452	4	US-09-248-796A-14553	Sequence 14553, A
41	78	12.9	1270	4	US-09-538-092-1321	Sequence 1321, App
42	77.5	12.9	474	4	US-09-543-681A-6752	Sequence 6752, App
43	77.5	12.9	693	3	US-08-235-836C-72	Sequence 72, Appl
44	77.5	12.9	785	4	US-09-248-796A-24492	Sequence 24492, A
45	77	12.8	422	4	US-09-248-796A-19321	Sequence 19321, A

ALIGNMENTS

RESULT 1
US-08-098-327E-20
Sequence 20, Application US/08098327E
Patent No. 6270771
GENERAL INFORMATION:
APPLICANT: GUERIN-MARCHAND, Claudine
TITLE OF INVENTION: DRUGS, Peptide
TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
HEPATIC STAGES OF P. FALCIPARUM BEARING EPTOPES CAPABLE
OF STIMULATING THE T LYMPHOCYTES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Machis
STREET: P. O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/098,327E
FILING DATE: 24-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 01286
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-045
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 92/13884
PUBLICATION DATE: 20-AUG-1992
US-08-098-327E-20
Query Match 100.0%; Score 603; DB 3; Length 117;

